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SEQUENCE LISTING

RECEIVED
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<110> Wright, David A.
Voytas, Daniel F.

<120> PLANT RETROELEMENTS AND METHODS RELATED THERETO

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<140> 09/965,553
<141> 2001-09-27

<150> 09/322,478
<151> 1999-05-28

<150> 60/087,125
<151> 1998-05-29

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gctctggta	aggagttta	ctccaaaccta	tatgatccag	aggaccacag	tccgaagtt	300
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accccggtca	tcttggcaga	gggagaggat	tatccagcct	actctcagta	cctcagca	420
cctccagacc	atgatgccat	cctttccgct	ctgtgtactc	cagggggacg	atttggatgt	480
aatgttgcata	gtgccccctg	gaagctgctg	cggaaggatc	tgatgacgct	cgcgccagaca	540
tggagtgtgc	tctcttattt	taaccttgc	ctgacttttc	acacttctga	tattaatgtt	600
gacagggccc	gactcaatta	tggcttgg	atgaagatgg	acctggacgt	gggcagcc	660
atttctcttc	agatcagtca	gatcgcccag	tccatca	ccaggcttgg	gttcccagcg	720
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tctatcacat	ttcaggggac	ccgcccac	cgcaccagag	cttcggcg	ggcatctgag	900
gctccttc	catcccagca	tccttc	ccttttccc	agagaccacg	gcctccactt	960
ctatccac	cagcac	atacatgc	ggacagatgc	tcagg	gtaccagg	1020
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Gln	Asp	Ser	Ile	Gln	Leu	Arg	Asn	Ile	Leu	Pro	Glu	Arg	Asn	Val	Glu
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Arg	Trp	Asp	Gln	Val	Leu	Thr	Arg	Leu	Pro	Glu	Lys	Trp	Ile	Asp	Val
								65		70				80	
Ala	Leu	Val	Lys	Glu	Phe	Tyr	Ser	Asn	Leu	Tyr	Asp	Pro	Glu	Asp	His
								85		90				95	
Ser	Pro	Lys	Phe	Trp	Ser	Val	Arg	Gly	Gln	Val	Val	Arg	Phe	Asp	Ala

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Glu Asp Tyr Pro Ala Tyr Ser Gln Tyr Leu Ser Thr Pro Pro Asp His			
130	135	140	
Asp Ala Ile Leu Ser Ala Leu Cys Thr Pro Gly Gly Arg Phe Val Leu			
145	150	155	160
Asn Val Asp Ser Ala Pro Trp Lys Leu Leu Arg Lys Asp Leu Met Thr			
165	170	175	
Leu Ala Gln Thr Trp Ser Val Leu Ser Tyr Phe Asn Leu Ala Leu Thr			
180	185	190	
Phe His Thr Ser Asp Ile Asn Val Asp Arg Ala Arg Leu Asn Tyr Gly			
195	200	205	
Leu Val Met Lys Met Asp Leu Asp Val Gly Ser Leu Ile Ser Leu Gln			
210	215	220	
Ile Ser Gln Ile Ala Gln Ser Ile Thr Ser Arg Leu Gly Phe Pro Ala			
225	230	235	240
Leu Ile Thr Thr Leu Cys Glu Ile Gln Gly Val Val Ser Asp Thr Leu			
245	250	255	
Ile Phe Glu Ser Leu Ser Pro Val Ile Asn Leu Ala Tyr Ile Lys Lys			
260	265	270	
Asn Cys Trp Asn Pro Ala Asp Pro Ser Ile Thr Phe Gln Gly Thr Arg			
275	280	285	
Arg Thr Arg Thr Arg Ala Ser Ala Ser Ala Ser Glu Ala Pro Leu Pro			
290	295	300	
Ser Gln His Pro Ser Gln Pro Phe Ser Gln Arg Pro Arg Pro Pro Leu			
305	310	315	320
Leu Ser Thr Ser Ala Pro Pro Tyr Met His Gly Gln Met Leu Arg Ser			
325	330	335	
Leu Tyr Gln Gly Gln Gln Ile Ile Gln Asn Leu Tyr Arg Leu Ser			
340	345	350	
Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg			
355	360	365	
Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu			
370	375	380	
Glu Pro Ser Gly Ala Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp			
385	390	395	400
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acctcacctc ctccttctcc aaattatgtt cagatggacg gggAACCGGC acaaagatc	180
acactagagg acttctctaa taccaccact cctcagttct ttacaagtat cacaaggccg	240
gaagtccaaag cagatctcct tactcaaggg aacctttcc atggcttcc aatgaagat	300
ccatatgcgc atcttagcctc atacatagag atatgcagca ccgttaaaat cgccggagtt	360

ccaaaagatg cgatactcct taacctcttt tcctttccc tagcaggaga ggcaaaaaga	420
tggttgact cctttaaagg caatagctt agaacatggg aagaagtatgt ggaaaaattc	480
ttaaaagaatg atttcccaga gtcaaagacc gtcgaacgaa agatggagat ttcttatttc	540
catcaatttc tggatgaatc ccttagcga gcactagacc atttccacgg attgctaaga	600
aaaacaccaa cacacagata cagcgagcca gtacaactaa acatattcat cgatgacttg	660
caactcttaa tcgaaacagc tactagaggg aagatcaagc tgaagactcc cgaagaagcg	720
atggagctcg tcgagaacat ggcggctagc gatcaagcaa tccttcatga tcacacttat	780
gttcccacaa aaagaagcct cttggagctt agcacgcagg acgcaacttt ggtacaaaac	840
aagctgtga cgaggcagat agaagccctc atcgaaacccc tcagcaagct gcctcaacaa	900
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gaacggccca ctagaacttt cggtgctaac atggagagaaa gaaccccaag gaaggataaaa	1440
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				20					25				30		
Gln	Asp	Ile	Glu	Gly	Ser	Ser	Tyr	Thr	Ser	Pro	Pro	Pro	Ser	Pro	Asn
					35				40				45		
Tyr	Ala	Gln	Met	Asp	Gly	Glu	Pro	Ala	Gln	Arg	Val	Thr	Leu	Glu	Asp
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Phe	Ser	Asn	Thr	Thr	Pro	Gln	Phe	Phe	Thr	Ser	Ile	Thr	Arg	Pro	
				65					70				75		80
Glu	Val	Gln	Ala	Asp	Leu	Leu	Thr	Gln	Gly	Asn	Leu	Phe	His	Gly	Leu
					85				90				95		
Pro	Asn	Glu	Asp	Pro	Tyr	Ala	His	Leu	Ala	Ser	Tyr	Ile	Glu	Ile	Cys
				100					105				110		
Ser	Thr	Val	Lys	Ile	Ala	Gly	Val	Pro	Lys	Asp	Ala	Ile	Leu	Leu	Asn
				115					120				125		
Leu	Phe	Ser	Phe	Ser	Leu	Ala	Gly	Glu	Ala	Lys	Arg	Trp	Leu	His	Ser
				130					135				140		
Phe	Lys	Gly	Asn	Ser	Leu	Arg	Thr	Trp	Glu	Glu	Val	Val	Glu	Lys	Phe
	145					150				155				160	
Leu	Lys	Lys	Tyr	Phe	Pro	Glu	Ser	Lys	Thr	Val	Glu	Arg	Lys	Met	Glu
					165				170				175		
Ile	Ser	Tyr	Phe	His	Gln	Phe	Leu	Asp	Glu	Ser	Leu	Ser	Glu	Ala	Leu
				180					185				190		
Asp	His	Phe	His	Gly	Leu	Leu	Arg	Lys	Thr	Pro	Thr	His	Arg	Tyr	Ser
				195					200				205		

Glu Pro Val Gln Leu Asn Ile Phe Ile Asp Asp Leu Gln Leu Leu Ile
 210 215 220
 Glu Thr Ala Thr Arg Gly Lys Ile Lys Leu Lys Thr Pro Glu Glu Ala
 225 230 235 240
 Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His
 245 250 255
 Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr
 260 265 270
 Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu
 275 280 285
 Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile
 290 295 300
 Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys
 305 310 315 320
 Arg Gly Thr His Glu Pro Gly Gln Cys Ala Ser Gln Gln Asp Pro Ser
 325 330 335
 Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly
 340 345 350
 Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe
 355 360 365
 Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly
 370 375 380
 Ser Ser Trp Thr Asn Lys Gly Asn Gln Tyr Lys Glu Gln Arg Asn Gln
 385 390 395 400
 Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln
 405 410 415
 Gln Glu Lys Pro Thr Lys Ile Glu Glu Leu Leu Gln Phe Ile Lys
 420 425 430
 Glu Thr Arg Ser His Gln Lys Ser Thr Asp Ala Ala Ile Arg Asn Leu
 435 440 445
 Glu Val Gln Met Gly Gln Leu Ala His Asp Lys Ala Glu Arg Pro Thr
 450 455 460
 Arg Thr Phe Gly Ala Asn Met Glu Arg Arg Thr Pro Arg Lys Asp Lys
 465 470 475 480
 Ala Val Leu Thr Arg Gly Gln Arg Arg Ala Gln Glu Glu Gly Lys Val
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 Arg Glu Ala Lys
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 atagccacgc caaaggacga tgccagggtt gtgatcaaat ttctgaagaa gaacatttt 240
 tcccgaaaa gaggcccacg agccttgatt agtgataggg gaacgcactt ctgcaacaat 300

cagttgaaga aagtccctgga gcactataat gtccgacata aggtggccac accttacac	360
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Asp Phe Met Gly Pro Phe Pro Ser Ser Tyr Gly Asn Val Tyr Ile Leu	
35 40 45	
Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Thr Pro	
50 55 60	
Lys Asp Asp Ala Arg Val Val Ile Lys Phe Leu Lys Lys Asn Ile Phe	
65 70 75 80	
Ser Arg Phe Gly Val Pro Arg Ala Leu Ile Ser Asp Arg Gly Thr His	
85 90 95	
Phe Cys Asn Asn Gln Leu Lys Lys Val Leu Glu His Tyr Asn Val Arg	
100 105 110	
His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln Ala Glu	
115 120 125	
Ile Ser Asn Arg Glu Leu Lys Arg Ile Leu Glu Lys Thr Val Ala Ser	
130 135 140	
Thr Arg Lys Asp Trp Ser Leu Lys Leu Asp Asp Ala Leu Trp Ala Tyr	
145 150 155 160	
Arg Thr Ala Phe Lys Thr Pro Ile Gly Leu Ser Pro Phe Gln Leu Val	
165 170 175	
Tyr Gly Lys Ala Cys His Leu Pro Val Glu Leu Glu Tyr Lys Ala Tyr	
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Trp Ala Leu Lys Leu Leu Asn Phe Asp	
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cgaactgtca ctgggtggcg aatgtgtatc gactatcgca agctgaatga agccacacgg	180
aaggaccatt tcccttacc tttcatggat cagatgctgg agagacttgc agggcaggca	240
tactactgtt tcttggatgg atactcggga tacaaccaga tcgcggtaga ccccaagat	300

caggagaaga cgccctttac atgcccctt ggcgtcttt cttacagaag gatgccattc
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<223> plant retroelement sequence

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				20				25					30		
Glu	Arg	Asn	Asp	Leu	Ile	Pro	Thr	Arg	Thr	Val	Thr	Gly	Trp	Arg	Met
					35			40				45			
Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn	Glu	Ala	Thr	Arg	Lys	Asp	His	Phe
					50			55				60			
Pro	Leu	Pro	Phe	Met	Asp	Gln	Met	Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ala
					65			70			75			80	
Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr	Ser	Gly	Tyr	Asn	Gln	Ile	Ala	Val
					85			90				95			
Asp	Pro	Arg	Asp	Gln	Glu	Lys	Thr	Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val
					100			105				110			
Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe	Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr
					115			120				125			
Phe	Gln	Arg	Cys	Met	Leu	Ala	Ile	Phe	Ser	Asp	Met	Val	Glu	Lys	Ser
					130			135				140			
Ile	Glu	Val	Phe	Met	Asp	Asp	Phe	Ser	Val	Phe	Gly	Pro	Ser	Phe	Asp
					145			150			155			160	
Ser	Cys	Leu	Arg	Asn	Leu	Glu	Arg	Val	Leu	Gln	Arg	Cys	Glu	Glu	Thr
					165			170				175			
Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	Cys	His	Phe	Met	Val	Arg	Glu	Gly
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Ile	Val	Leu	Gly	His	Lys	Ile	Ser								
					195			200							

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<400> 13

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ccattcgggg	aagccttaca	gcagatcccc	ctctactcca	aatttatgaa	agacatcctc											
accaagaagg	ggaagtataat	tgacaacgag	aatattgtgg	taggaggcaa	ttgcagtgc											
ataatacaaa	ggattctacc	caagaatttt	aaagaccccc	gaagtgttac	catcccgtgc											
accattggga	aggaagccgt	aaacaaggcc	ctcattqatc	taqqaqcaaq	tatcaatctq											

60
 120
 180
 240
 300
 360

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gatgtcagtt	ttctcgagac	accaaagact	tcgctagaaa	aagcaatggt	aaatcattta	780
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 20 25 30
 Phe Lys Gly Leu Glu Ile Thr Met Pro Phe Gly Glu Ala Leu Gln Gln
 35 40 45
 Met Pro Leu Tyr Ser Lys Phe Met Lys Asp Ile Leu Thr Lys Lys Gly
 50 55 60
 Lys Tyr Ile Asp Asn Glu Asn Ile Val Val Gly Gly Asn Cys Ser Ala
 65 70 75 80
 Ile Ile Gln Arg Ile Leu Pro Lys Lys Phe Lys Asp Pro Gly Ser Val
 85 90 95
 Thr Ile Pro Cys Thr Ile Gly Lys Glu Ala Val Asn Lys Ala Leu Ile
 100 105 110
 Asp Leu Gly Ala Ser Ile Asn Leu Met Pro Leu Ser Met Cys Lys Arg
 115 120 125
 Ile Gly Asn Leu Lys Ile Asp Pro Thr Lys Met Thr Leu Gln Leu Ala
 130 135 140
 Asp Arg Ser Ile Thr Arg Pro Tyr Gly Val Val Glu Asp Val Leu Val
 145 150 155 160
 Lys Val Arg His Phe Thr Phe Pro Val Asp Phe Val Ile Met Asp Ile
 165 170 175
 Glu Glu Asp Thr Glu Ile Pro Leu Ile Leu Gly Arg Pro Phe Met Leu
 180 185 190
 Thr Ala Asn Cys Val Val Asp Met Gly Lys Gly Asn Leu Glu Leu Thr
 195 200 205
 Ile Asp Asn Gln Lys Ile Thr Phe Asp Leu Ile Lys Ala Met Lys Tyr
 210 215 220
 Pro Gln Glu Gly Trp Lys Cys Phe Arg Ile Glu Glu Ile Asp Glu Glu
 225 230 235 240
 Asp Val Ser Phe Leu Glu Thr Pro Lys Thr Ser Leu Glu Lys Ala Met
 245 250 255
 Val Asn His Leu Asp Cys Leu Thr Ser Glu Glu Glu Glu Asp Leu Lys
 260 265 270
 Ala Cys Leu Glu Asn Leu Asp Gln Glu Asp Ser Ile Pro Glu
 275 280 285

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 Gly Gln Arg Lys Asp Lys Val Phe His Ala Ile Tyr Tyr Ala Ser Lys
 20 25 30
 Val Leu Asn Glu Ala Gln Leu Asn Tyr Ala Thr Thr Glu Lys Glu Met
 35 40 45
 Leu Ala Ile Val Phe Ala Leu Glu Lys Phe Arg Ser Tyr Leu Ile Gly
 50 55 60

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<213> Artificial Sequence

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 Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln
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<400> 47		
cgactcgagc tccatagcga tg		22
<210> 48		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		

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<223> primer

<400> 48
cggattgggc cgaaaatggac cgaa 24

<210> 49
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<212> DNA
<213> Arabidopsis thaliana

<400> 49
gaggacttgg ggggcaaa 18

<210> 50
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<221> VARIANT
<222> 2-3, 5-7, 9-12
<223> Xaa = Any Amino Acid

<400> 50
Cys Xaa Xaa Cys Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Cys
1 5 10

<210> 51
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<400> 51
Leu Ile Asp Leu Gly Ala
1 5

<210> 52
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 52
Lys Thr Ala Phe
1

<210> 53
<211> 8
<212> PRT
<213> Artificial Sequence

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<220>
<223> consensus sequence

<221> VARIANT
<222> 2
<223> Xaa = Pro or Ser

<400> 53
Met Xaa Phe Gly Leu Cys Asn Ala
 1           5

<210> 54
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 1
<223> Xaa = Val, Ile, or Met

<221> VARIANT
<222> 9
<223> Xaa = Ser or Trp

<221> VARIANT
<222> 10
<223> Xaa = Val or Ile

<400> 54
Xaa Glu Val Phe Met Asp Asp Phe Xaa Xaa
 1           5           10

<210> 55
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 12
<223> Xaa = Ile or Val

<400> 55
Phe Glu Leu Met Cys Asp Ala Ser Asp Tyr Ala Xaa Gly Ala Val Leu
 1           5           10           15
Gly Gln Arg

<210> 56
<211> 27
<212> PRT

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<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 4

<223> Xaa = Thr or Ile

<221> VARIANT

<222> 8

<223> Xaa = Leu or Met

<221> VARIANT

<222> 13

<223> Xaa = Phe or Tyr

<221> VARIANT

<222> 15

<223> Xaa = Leu or Phe

<221> VARIANT

<222> 19

<223> Xaa = Arg or Lys

<221> VARIANT

<222> 23

<223> Xaa = Ile or Val

<221> VARIANT

<222> 26

<223> Xaa = Arg or Lys

<400> 56

Tyr Ala Thr Xaa Glu Lys Glu Xaa Leu Ala Ile Val Xaa Ala Xaa Glu

1

5

10

15

Lys Phe Xaa Ser Tyr Leu Xaa Gly Ser Xaa Val

20

25

<210> 57

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 4, 6-7, 11-40, 43

<223> Xaa = Any Amino Acid

<400> 57

His Cys His Xaa Ser Xaa Xaa Gly Gly His Xaa Xaa Xaa Xaa Xaa Xaa

1

5

10

15

Xaa Xaa

20

25

30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Asp Xaa Cys Gln Arg

35

40

45

<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 6
<223> Xaa = Ile, Val, or Met

<400> 58
Trp Gly Ile Asp Phe Xaa Gly Pro
1 5

<210> 59
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 7
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 10
<223> Xaa = Ala or Val

<400> 59
Pro Tyr His Pro Gln Thr Xaa Gly Gln Xaa Glu
1 5 10

<210> 60
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> misc_feature
<222> 11, 12
<223> n = A,T,C or G

<400> 60
atttggggra nnt

<210> 61
<211> 9
<212> PRT
<213> Artificial Sequence

13

<220>
<223> consensus sequence

<221> VARIANT
<222> 5, 8
<223> Xaa = Arg or Lys

<400> 61
Gln Met Ala Ser Xaa Lys Arg Xaa Ala
1 5

<210> 62
<211> 6
<212> PRT
<213> Pisum sativum

<400> 62
Ala Ser Lys Lys Arg Lys
1 5